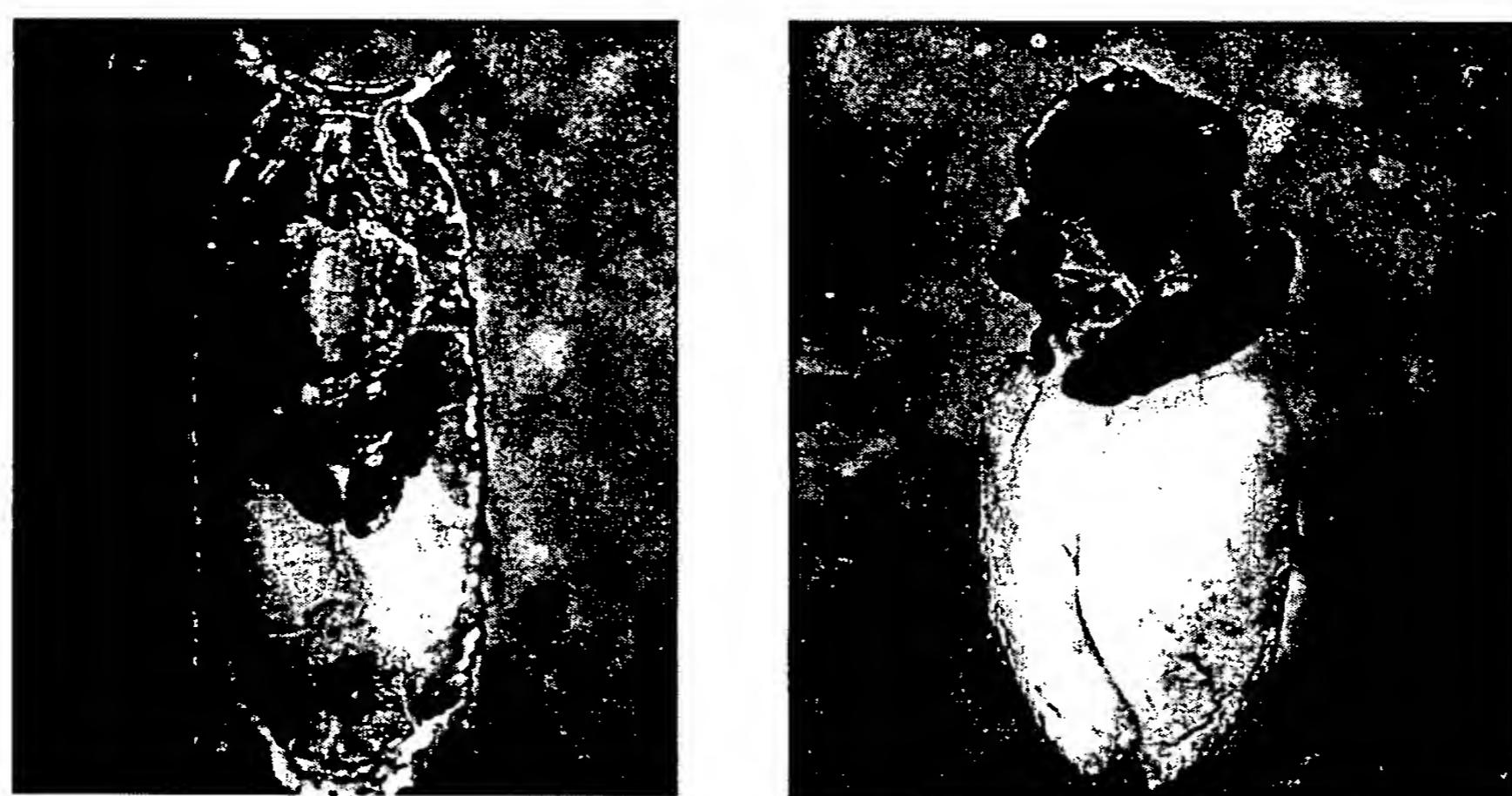


Figure 1

A



B



C

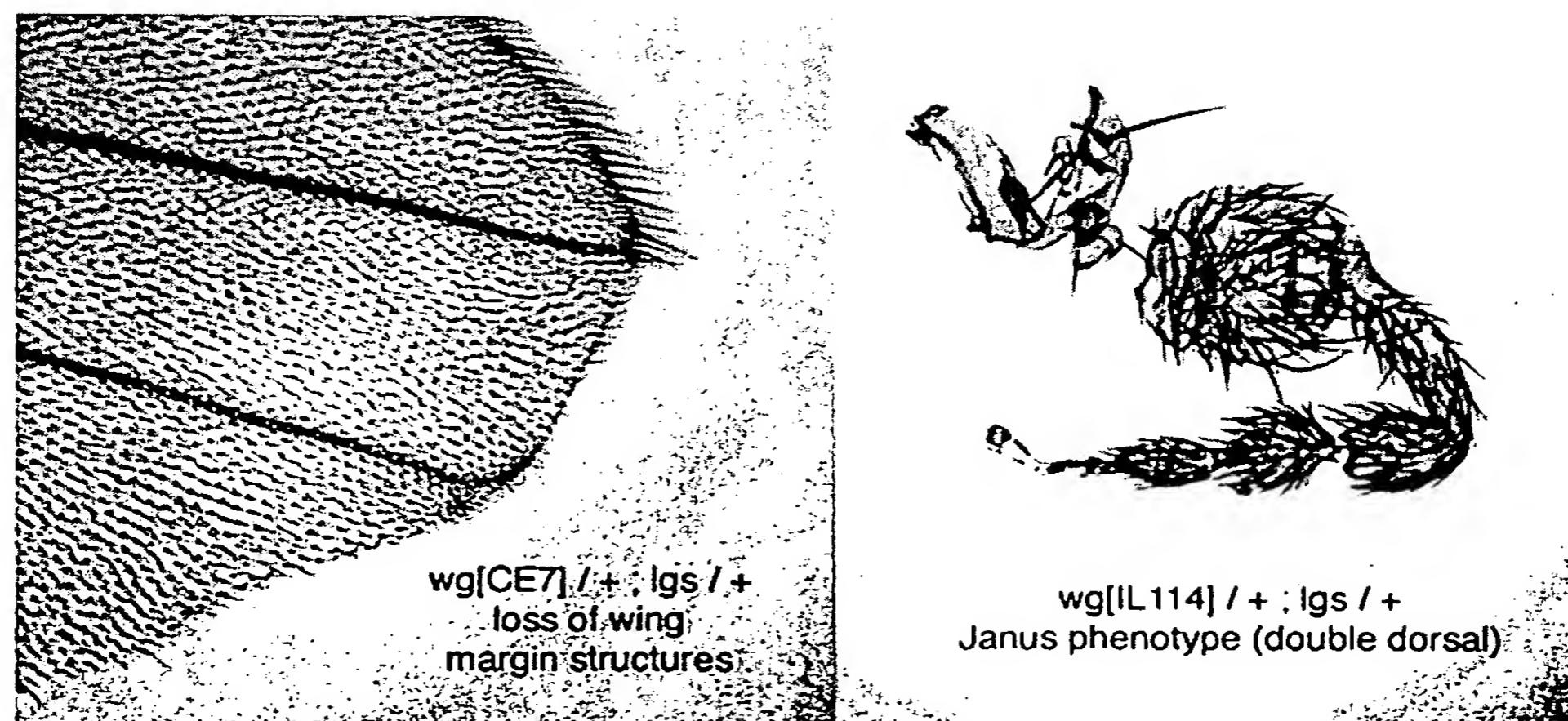


Figure 2

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CCTGCTAACATAACGCCACCGTTAACCGAGGACATTGGGCTATAAGCCAAAATTTC	120	TGTGCTGGAAAGGCGATCTCAAACACCACTGAGGTCTGGACAAAACCTCAGGAAATCATG C W E G G S S N T S R S G Q N S R N H V	3120 465
TTAGCTTAATACGATGCTCCGAAAGTGTATTGCAATTGACATATAACATAAAATTGTCAC	180	TAGACAGTATCAGTACATCAGCGAGTCACAGGCAATAAAGATACTGAGCAGCTGG D S I S T S S E S O A I K I L E A A G V	3180 485
ATAGAATAGGAGAATTCCACATACAAATACAAAATACAAAATCCTCCAGTAAAATTAA	240	TTGATTGGACAGGTCACAAAAGGAAGGAGTCTGGCTGACAACGAAACTGAAAACATTG D L G Q V T K G S D P G L T T E N N I V	3240 505
AACGATATGTTGCTTCGCTGAGTCTGGCTAAATATGCTTAATTGGCTTCGCCACTTC	300	TATCACTGCAAGGAGTAAAGGTTCCAGACGAAAACCTTACACCACACCGGCAACATC S L Q G V K V P D E N L T P Q Q R Q H R	3300 525
GTGAGTGCTGGCTGAGTCTGGCTAAATATGCTTAATTGGCTTCGCCACTTC	360	GGGAAGAACAGTGGCAAAAATAAAAAAATGAATCAATTCTTTCTGAAAATGAGA E E Q L A K I K K M N Q L F P E N E N	3360 545
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M P R S P	5	GGATGTCGGGTTGGCGAGGCGATCTATTATAAACTCCGAGTGCACACTGCAATATGC M S G G G G S I I I N P T M R Q L H M P	3480 585
CAACCAAACACAGCCGAACCAAACCTCCGATGCCCTCTCAACAGTGCATCTGATCAA T Q Q Q P Q P N S D A S S T S A S G S N	540	CAOGTAAACCCAAAATCGAGCTCTTATCGCGACAACTTCAGGACTTCAGGAGATGTA G N A K S E L L S A T S S G L S E D V M	3540 605
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TATTCGGCTTCACTTGTGTTAATCATTTAATTGTTGCTATACTTACAAATT AGTTTAAACTGAAACTTGACTAAACTCGGAAGCTGGATCAAAACAGACATTTC T T G G A C C G T A A T T A A G G T C A T A A A A T T A T T A A T T A A T T A A T G 1080	1080	TCCAGAGATCTGGTCAGTACCAATAGCCACTCAATCGCCAATCCCTGAGTC Q R S A S V P I A T Q S P N P S S P N N	4080 785
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GAACACTATAGGATATCTCTGCTTTAATTATTAGAAATTAGAATAT 1460	1460	TGATAACATGAAAAGTAGGGACCAAGCCCACAGGGTCAGGGTCACCG D N M K S R R P S P Q G Q R S P V N S L	4740 911
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CTATAAACTTTGAGCTATCTGATACTGCAAGCTACTAAAATGATTAGTTAG 1640	1640	ACAGATGGAGGAAATATTAAATTAAACGTTT Q M E	4920 954
ATGGGTGTAATTGTTAGGAAGTTTCATTTAGAAGAAATGTGATTATTAAAC 1700	1700	TTTCAGCGTCAGCATCGGCAAGGTCAGGTTGATCGGACCA R Q A S A Q G G S V Q F S R R S D N	4980 972
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AAAGTGCTTAAATTGAGGAAATTCCACGGGTTCAAATACTAACCGGTTT 1820	1820	GATCCAATCTCTTGGCACAATGTCCTAAACACTAACAGTTGG D P I S S L A Q M S Q Q L T S C V S S M	5100 1012
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ATCACAGCAGATTTCCTGCTATATAGAAGTCGGCTACACTCTCTGGC 1940	1940	AATATTGAGCATGGAAATTTCGGGACTAGATGGTCAGGA A A T T G G C T T A A T T G G C T T A A T T G G C T T A A T T G G C T T A A T T G G C T T 1052	5220 1052
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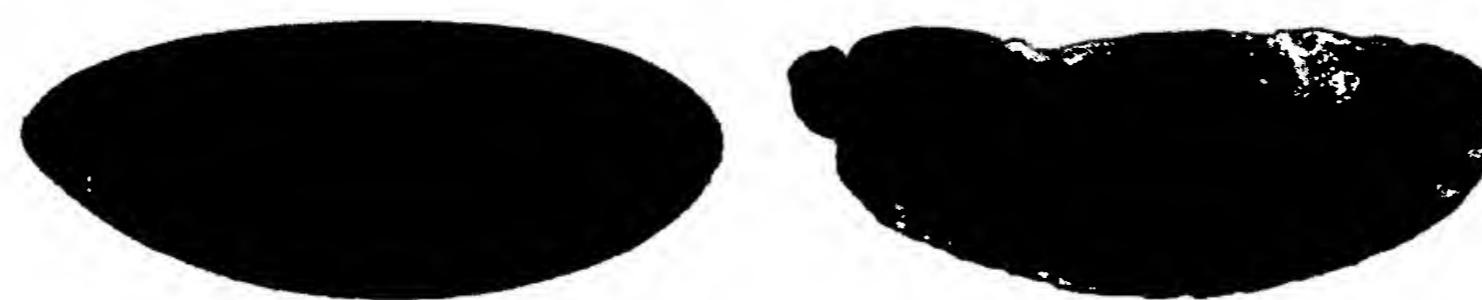
Figure 2: *legless*

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T N N P G A S N G I N F F Q N C N Q M S	1252
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I V D E E G G L P G H D G S H N I G Q P	1272
TCTATGATAACGGGCAATGGTCCACATGCCATOCGGCCTAATGTAAATGGTCAACCA	5940
S M I R G M R P H A M R P N V M G A R M	1292
CCACCCGTTAACAGGCAAATTCACTTTCAGTTCACAGTCATCGGATGGTATTGACTGTGTCGGG	6000
P P V N R Q I Q F A Q S S D G I D C V G	1312
GATCCGTCACTATTTCCTAACTAACGCTTCTGCAACAGCGCTGGACACACATGTTGGA	6060
D P S S F F T N A S C N S A G P H M F G	1332
TCAGCACACAGGCCAATCAGCTTAAGACACAACACATAAAAGAACATACTAGTOGAATG	6120
S A Q Q A N Q P K T Q H I K N I P S G M	1352
TGTCAAAACCAATCGGGACTTGCAGTGGCACAAOGGCAGATCCAACTOCATGGCAAGGA	6180
C Q N Q S G L A V A Q G Q I Q L H G Q G	1372
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H A Q G Q S L I G P T N N N L M S T A G	1392
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S V S A T N G V S G I N F V G P S S T D	1412
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L K Y A Q Q Y H S F Q Q Q L Y A T N T R	1432
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S Q Q Q Q H M H Q O H Q S N M I T M P P	1452
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N L S P N P T F F V N K	1465
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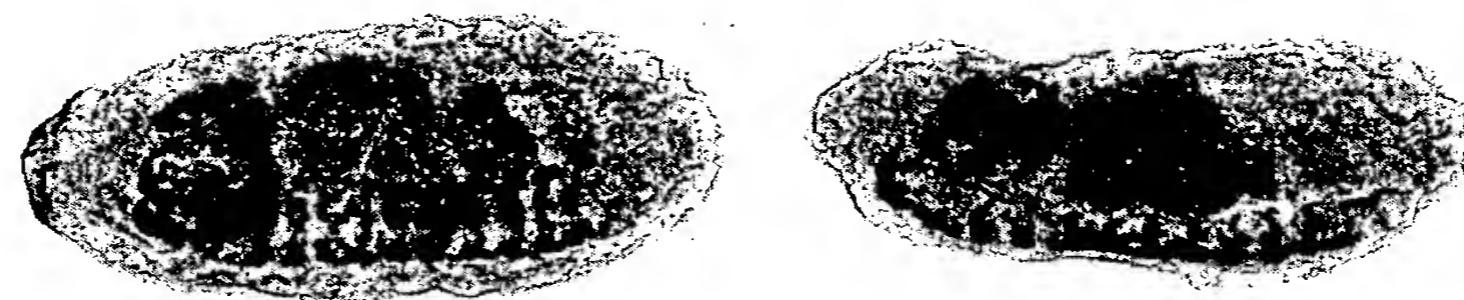
AAAAAAAAAA 6909

Figure 3

A



yw x lgs anti-sense



yw x lgs sense

B

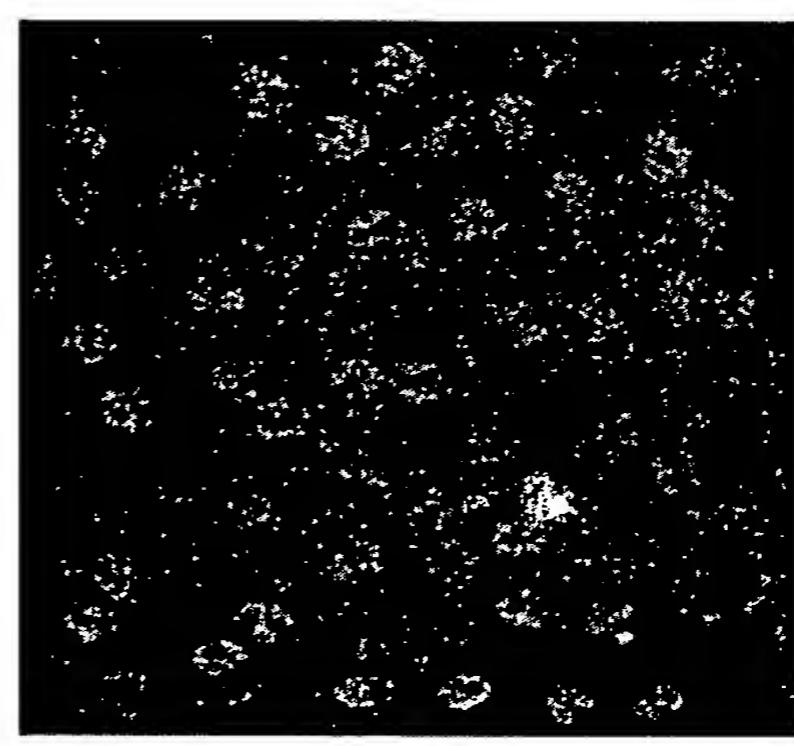
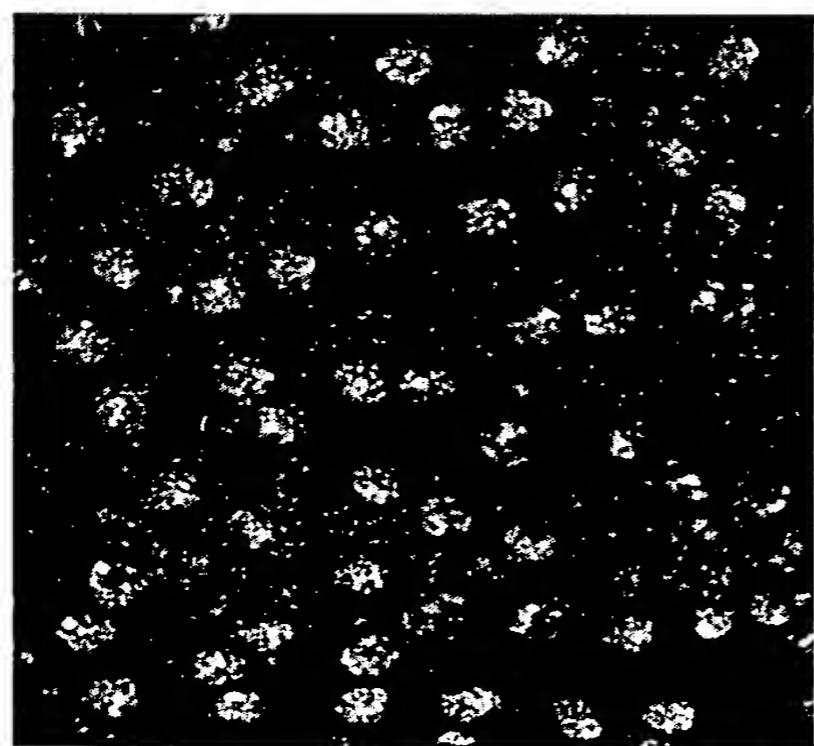


Figure 4

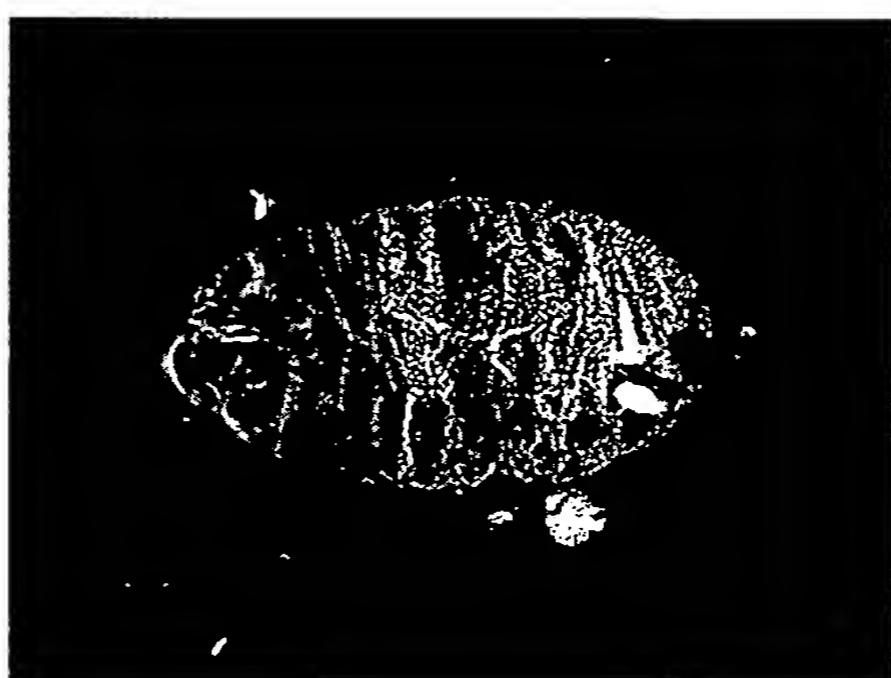
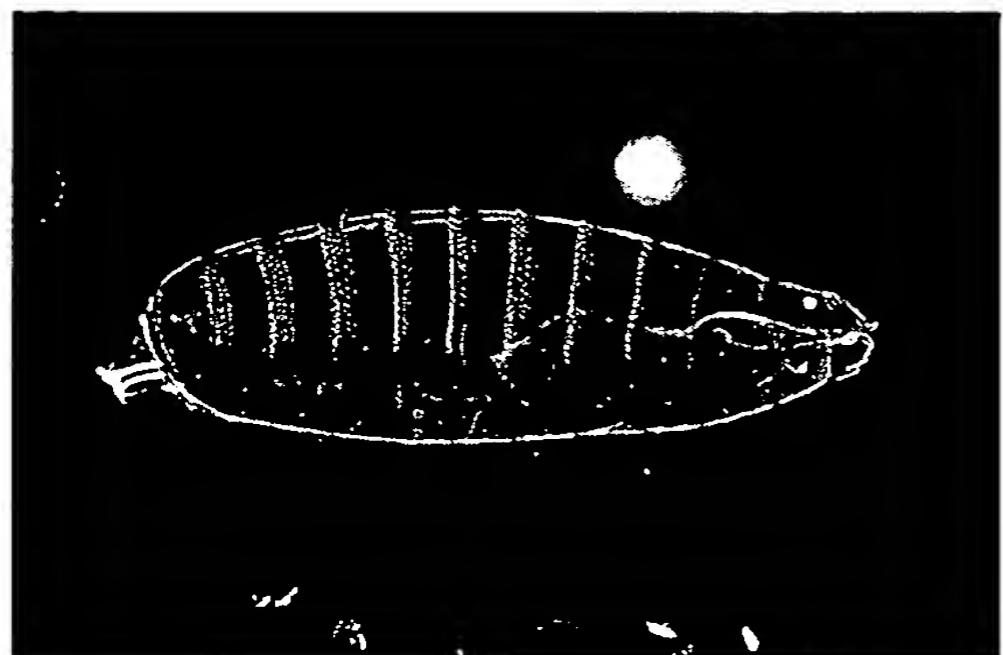
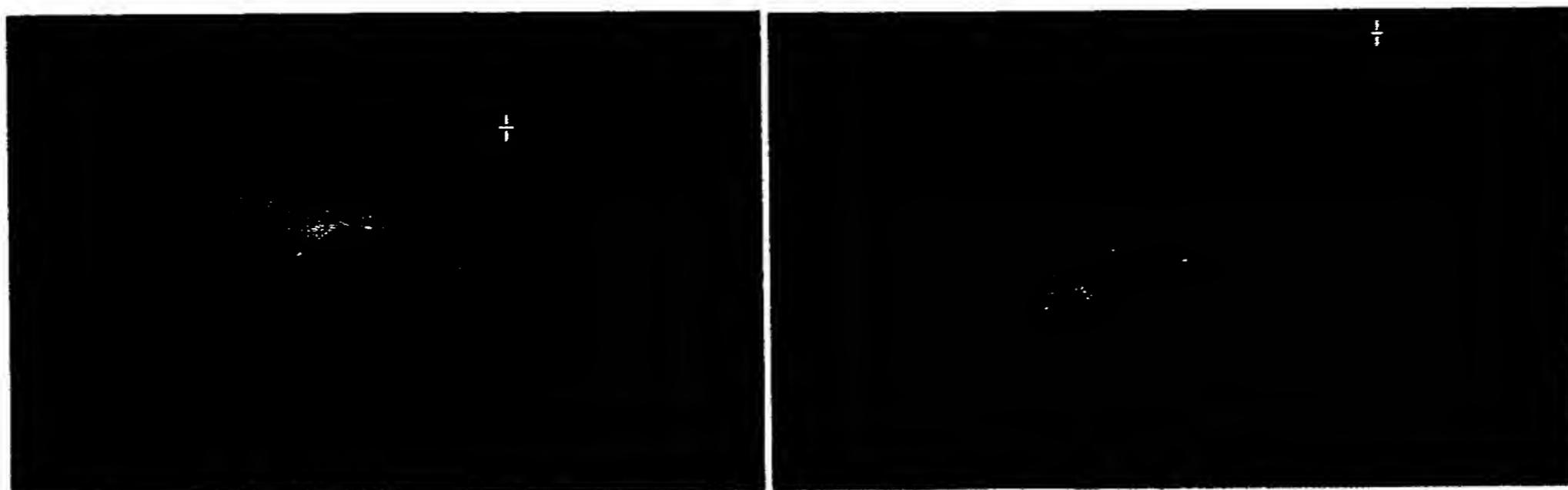


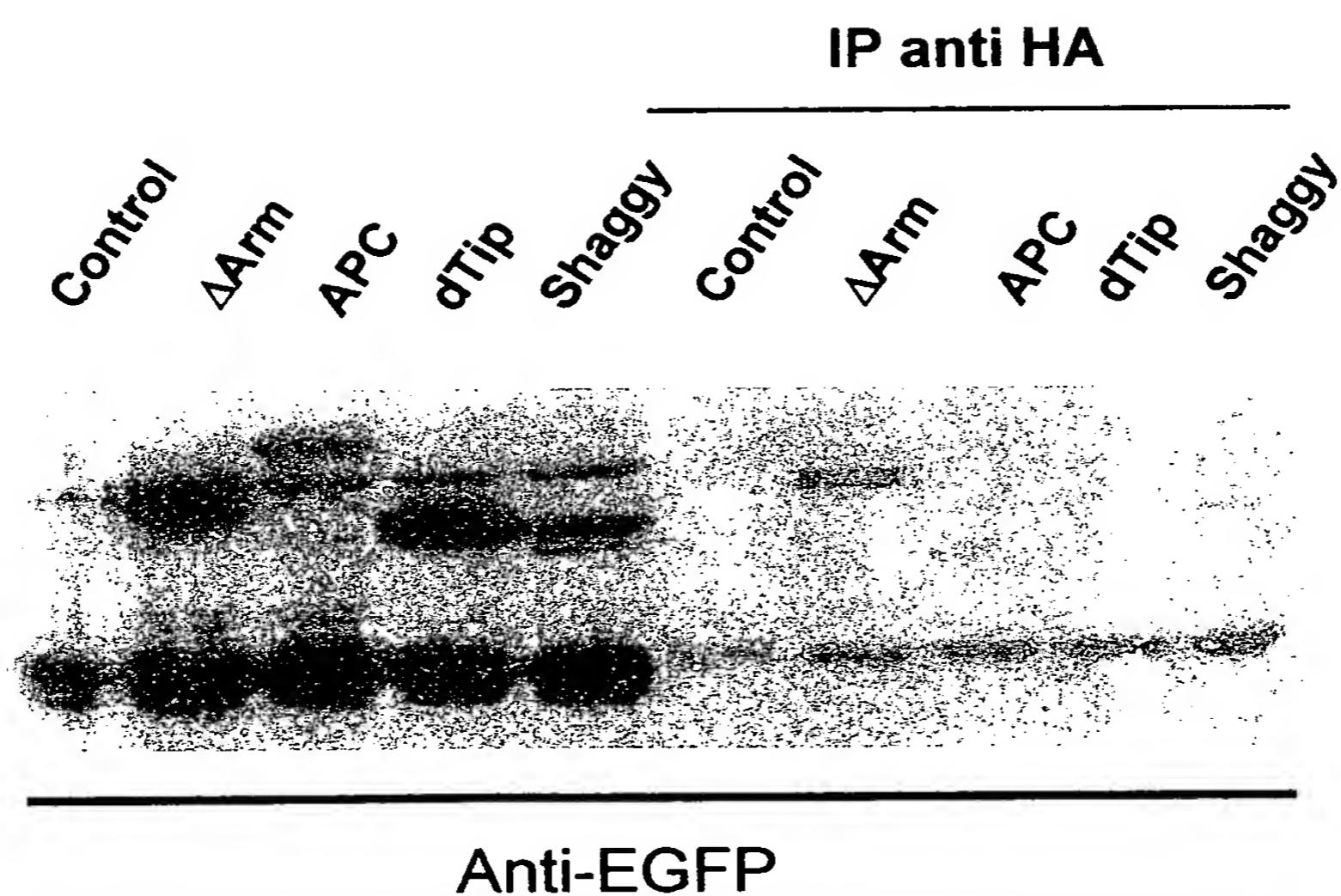
Figure 5

A

EGFP-Lgs EGFP-Lgs + pcDNA3-Arm-NLS



B



5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	ΔArmC	Δβ-Cat	Pan
PREY fusions: pJG4-5	Igs364-555					+		
	Igs1-385					-		
	Igs1-732					+		
	Igs364-1090					+		
	Igs726-1464					-		
	Igs1-1464				-	+	n.d.	+
	BCL9 199- 392					+	n.d.	
	BCL91-1426					+	+	
	Dco+	-						
	DAxin	(+)				+		
	ΔArmC	+	+	+				+
	β-Cat	+	+	+				
	Pan	+				+		
	pJG4-5	-	-			-	-	

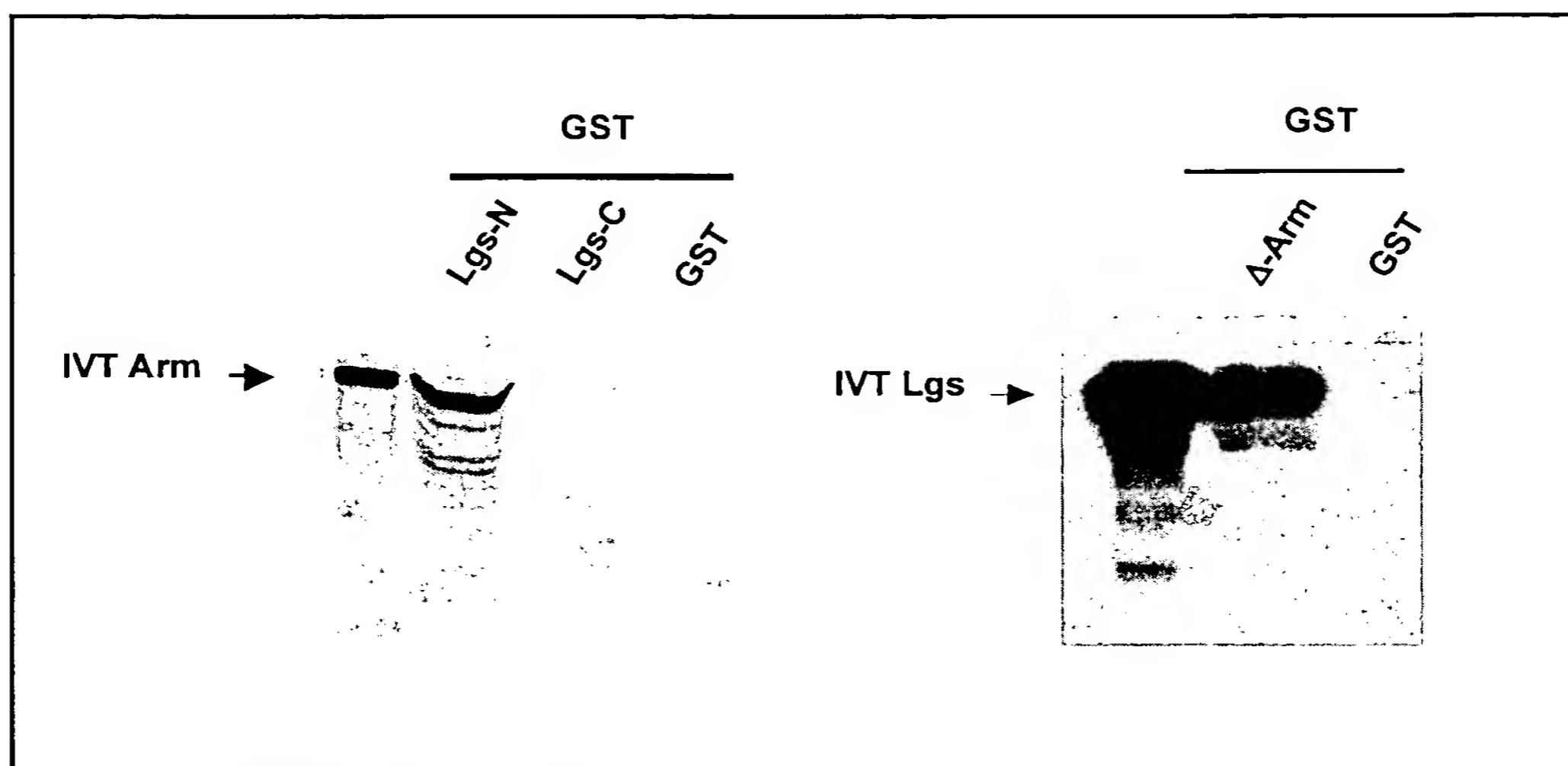
+: interaction seen in yeast two-hybrid assay

-: no interaction seen in yeast two-hybrid assay

n.d.: not done

numberings refer to amino acid positions.

5D



5E

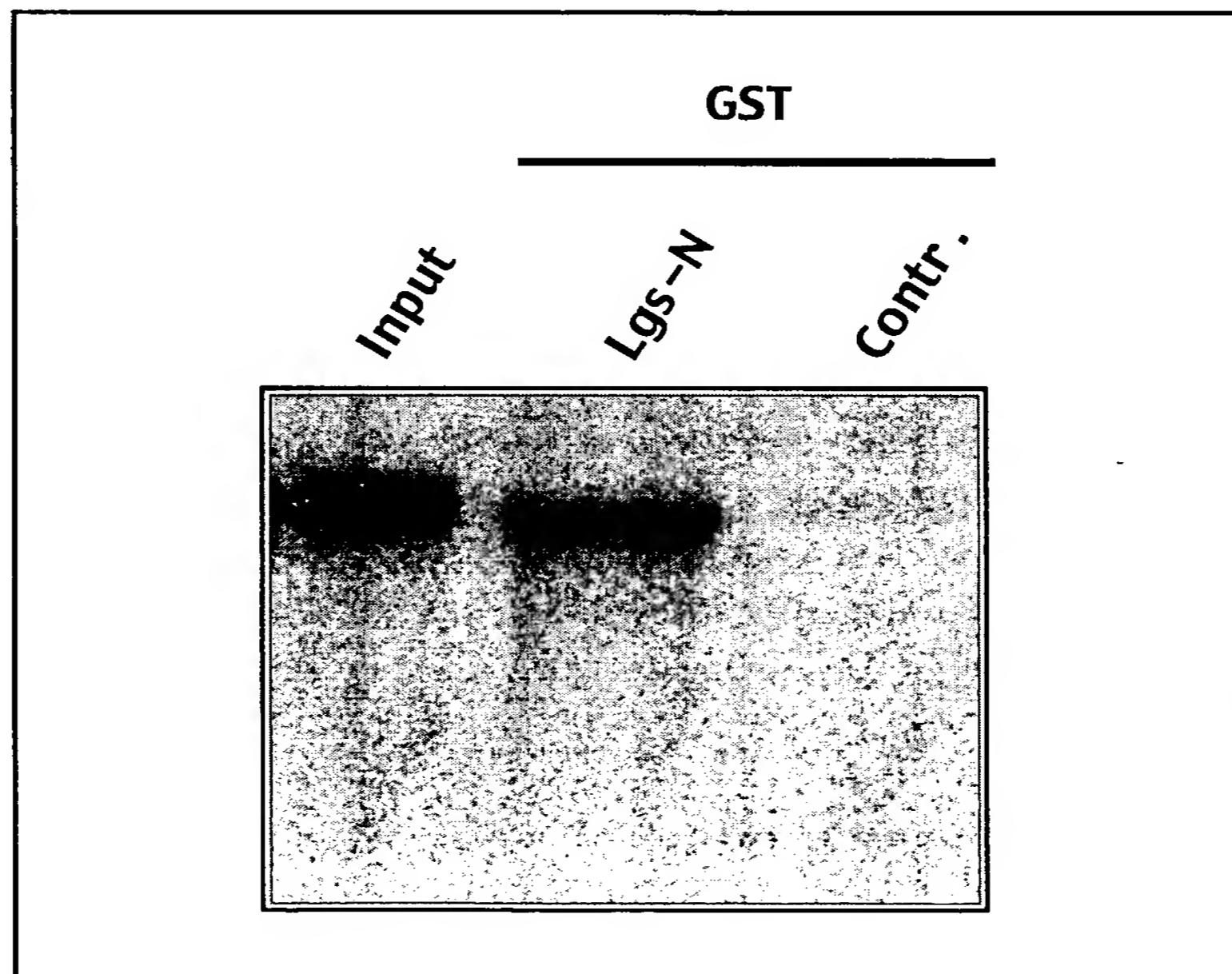


Figure 6

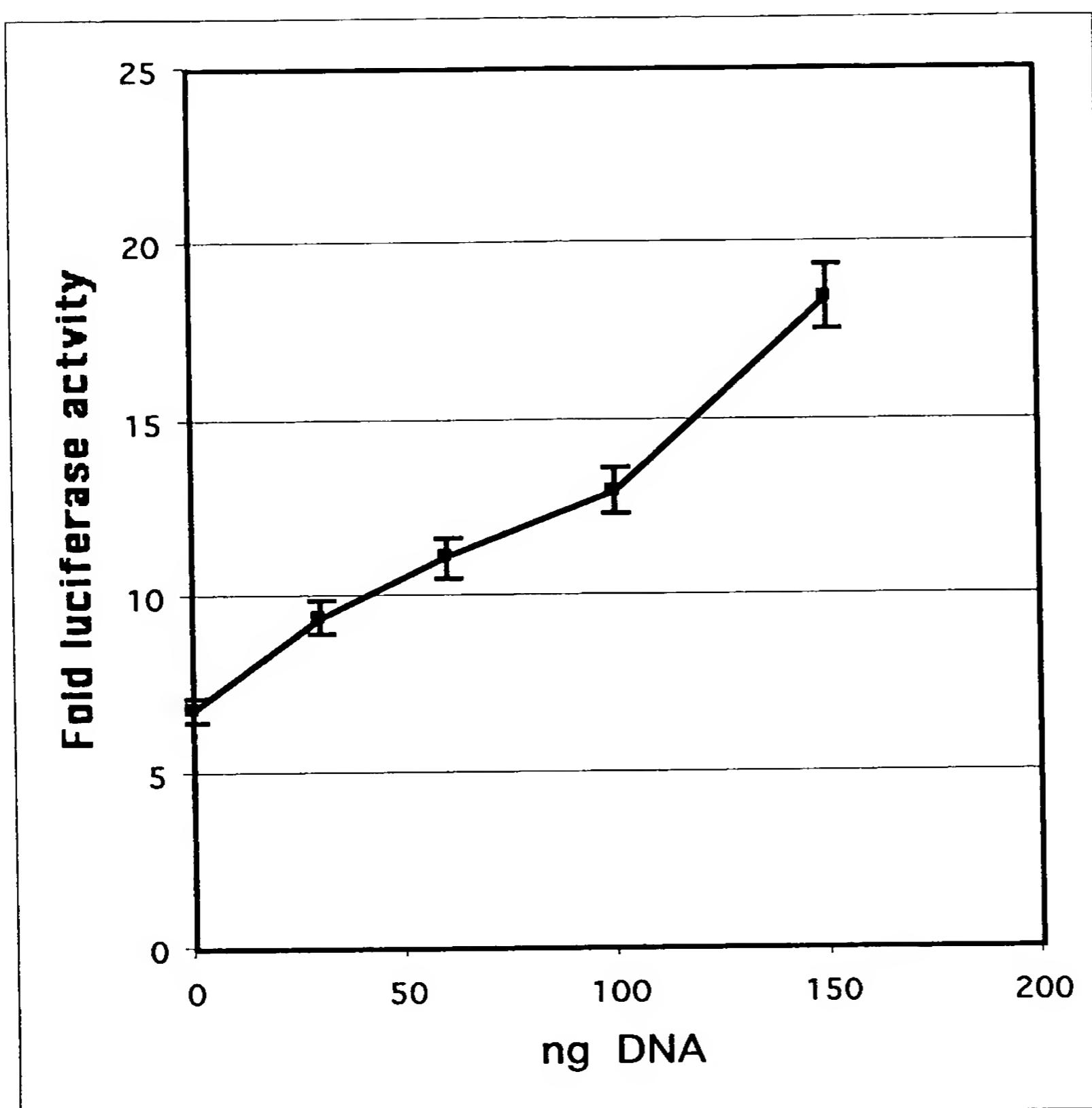
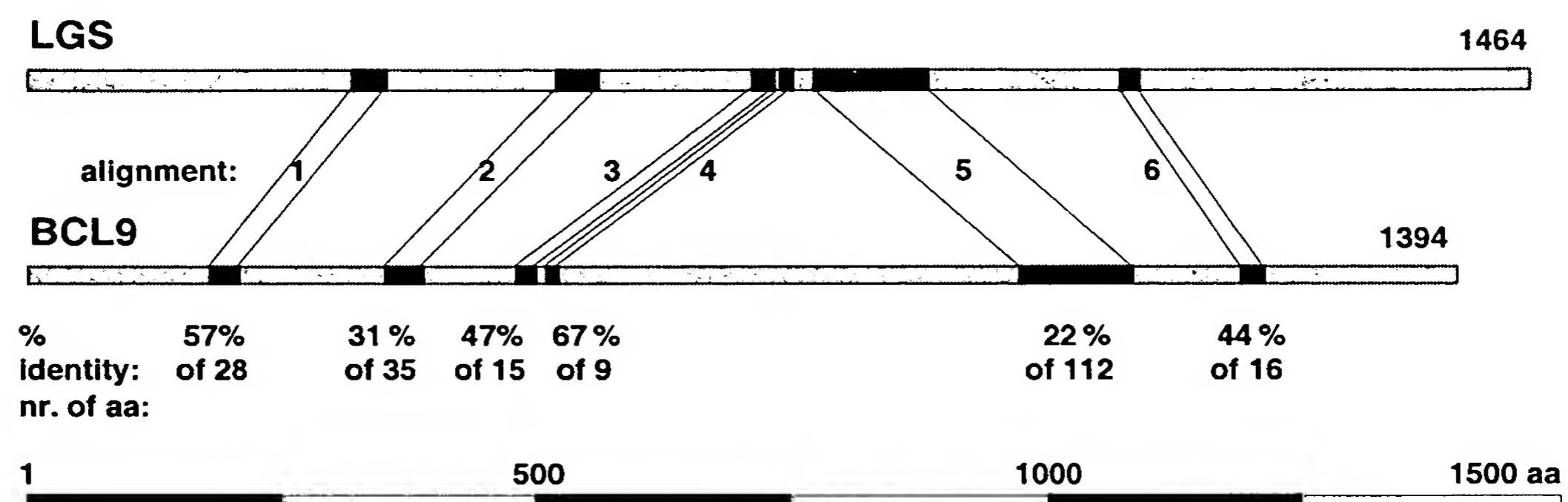


Figure 7

A



7B

Sequence homology domain 1: 57.1% identity in 28 aa

	320	330	340
LGS	IFVFSTQLANKGAESVLSGQFQTIIAYH		
	180	190	200
BCL9	VYVFSTEMANKAAEAVLKGQVETIVSFH		

Sequence homology domain 2: 31.4% identity in 35 aa

	520	530	540
LGS	ENLTPQQRQHREEQLAKIKKMNQFLFPENENSGA		
	350	360	370
BCL9	DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA		
	470	480	380

Sequence homology domain 3: 46.7% identity in 15 aa

	710	720
LGS	QMEWSKIHQFFER	
	470	480
BCL9	QIAWLKLQQEFYEEK	

Sequence homology domain 4: 66.6% identity in 9 aa

	760
LGS	LQGPPPPYH
	520
BCL9	VRGPPPPYQ

Sequence homology domain 5: 22.3% identity in 112 aa

	770	780	790	800	810	820
LGS	SASVPIATQSPNPSSPNLNSLPSPRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQA					
	970	980	990	1000	1010	1020
BCL9	GPPPPTASQPASVNIPGSLPSSTPYTMRPEPTLSQNPLSIM-MSRMSKFAMPSSTPLYHD					
	830	840	850	860	870	
LGS	GTTTVLSANKNCFQADTPSPSNQNRSRNTGSSVLTHNLSSNPSTPLSHLSP					
	1030	1040	1050	1060	1070	
BCL9	AIKTVASSDDDSPPARSPNLPSSMNNMPGMGINTQNPRIISGPNPVVPMPTLS					

Sequence homology domain 6: 43.8% identity in 16 aa

	1080
LGS	NPKMCVAGGPNGPPGF
	1190
BCL9	DAALCKPGPGGGPDSF
	1200

Figure 8

A

ATGCATTCCAGTAACCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
GAGTAGCCCTAAGTCAGGAGGTGATGGTCCGTCCCCCTACAGTGA
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GTCTTCCACATCCAGAACATTCTAACAAACAAGACAGAGAGAACAC
AGCGCCTCTGAACACACAGATATCTGCCCTCGGAATGATCCGAAACCTC
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ATACCAGATGACCCCTAGTGAAGGCTGGCACCTGGGGTACAGAGCCAT
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GATGGTCGAAATTTCCTCTGGCCAGGGCATTTCAGCGGTCCCTGGCCG
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AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCAGGGATGGCCATGGAA
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Figure 8A

ATGGGCOCTGGTCGGGAACCTGAGTTGGGATGGTCCTAGTGGGATGAA
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CTCAGAAGATGAGAGAGGGCTGGGGCGGGCCCTGAGGAGATGCTGAAATT
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT
GCCATTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCAGACCAT
TCCTTCCCAGTCTCAGGGTCCAGGCAGCAACAGTGGCTGCGGAATCTC
AGAGAACCAATTGGGCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT
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CTCCTCCAGTTCAGCGCGGCGTGGGCGGAAGGCCCTGGATATATCTGTG
GCAGGCAGGCCAGGTGCATTCCCCAGGCATTAACCCCTCTGAAGTCTCCCAC
GATGCACCAAGTCCAGTCACCAATGCTGGCTGCCCTGGGAACCTCA
AGTCOOCCCCAGACTCCATCGCAGCTGGCAGGCATGCTGGCGGGCCAGCT
GCTGCTGCTCCATTAAAGTCCCCCTGTTTGGGGTCTGCTGCTGCTTC
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CCTCTTCTCCAAAACCTCCCCCTCAGAGTCCTGGGATCCCTCAAACCAT
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AGGTGGCCCCCCCACCTCCTACAGCCAGGCCAGCCTGCCTCTGTGAATATCC
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GCTCAGATGACGACTCCCCCTCCAGCTCGTTCTCCAACTTGCCATCAATG
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CCCAAAGTTCAGCAGATGCAGCACTTGCAAGCCTGGAGGGCCCCGGGGT
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ACCACCAAGCCTTCTCCAACAAGGCATGATGGGACCTCACCATGGATGA
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Figure 8B

B

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PRSSTPSHGQTATEPTPAQKTPAKVVVFSTEMANKAAEAVLKGQVETI
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KPEGPIQAMMAQSQSLGKGPGRPTDVGAPFGPQGHARDVPFSPDEM/PPSM
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Figure 9

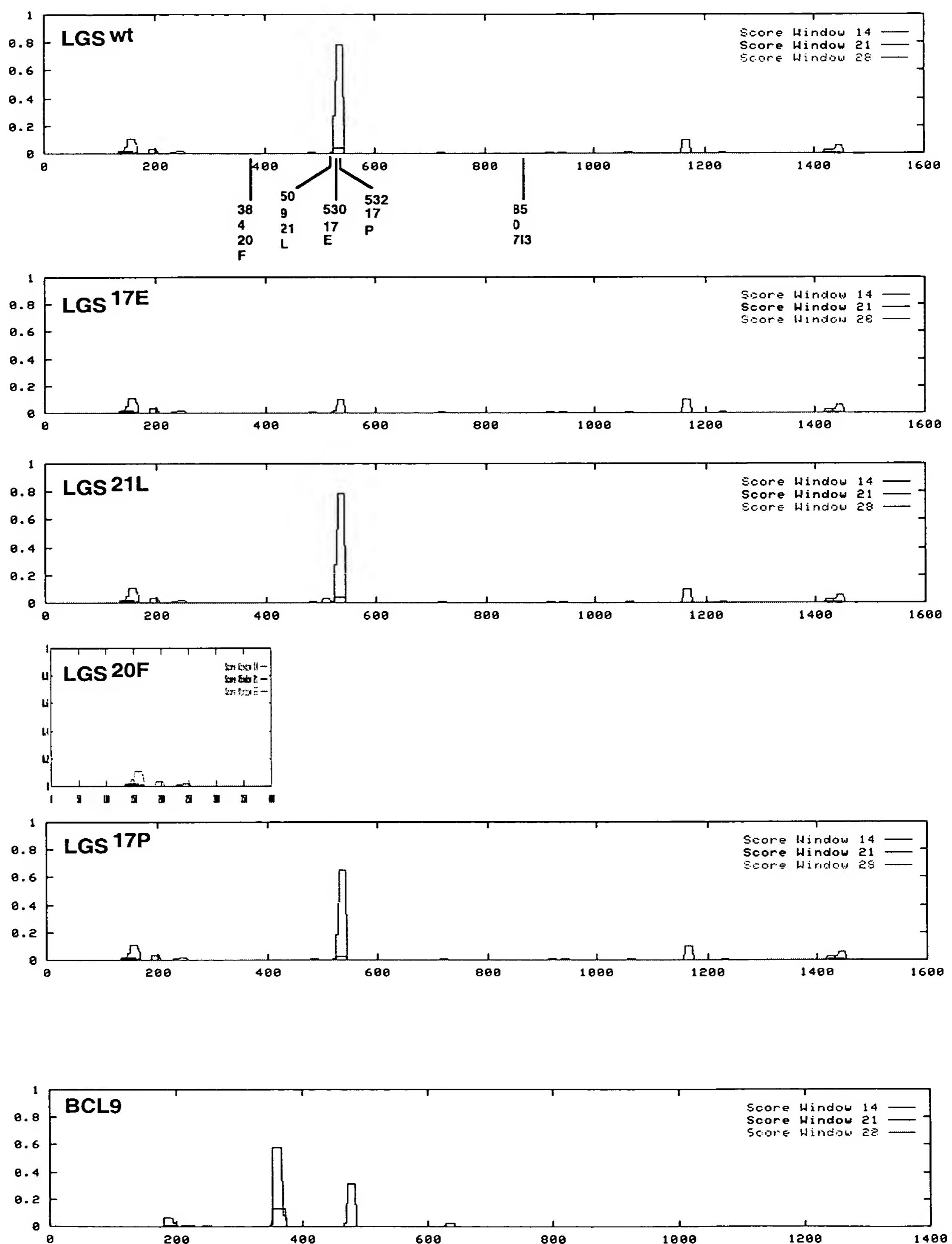


Figure 10

A

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GTAC

Figure 10

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B

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Figure 11

A



B



Figure 12

A

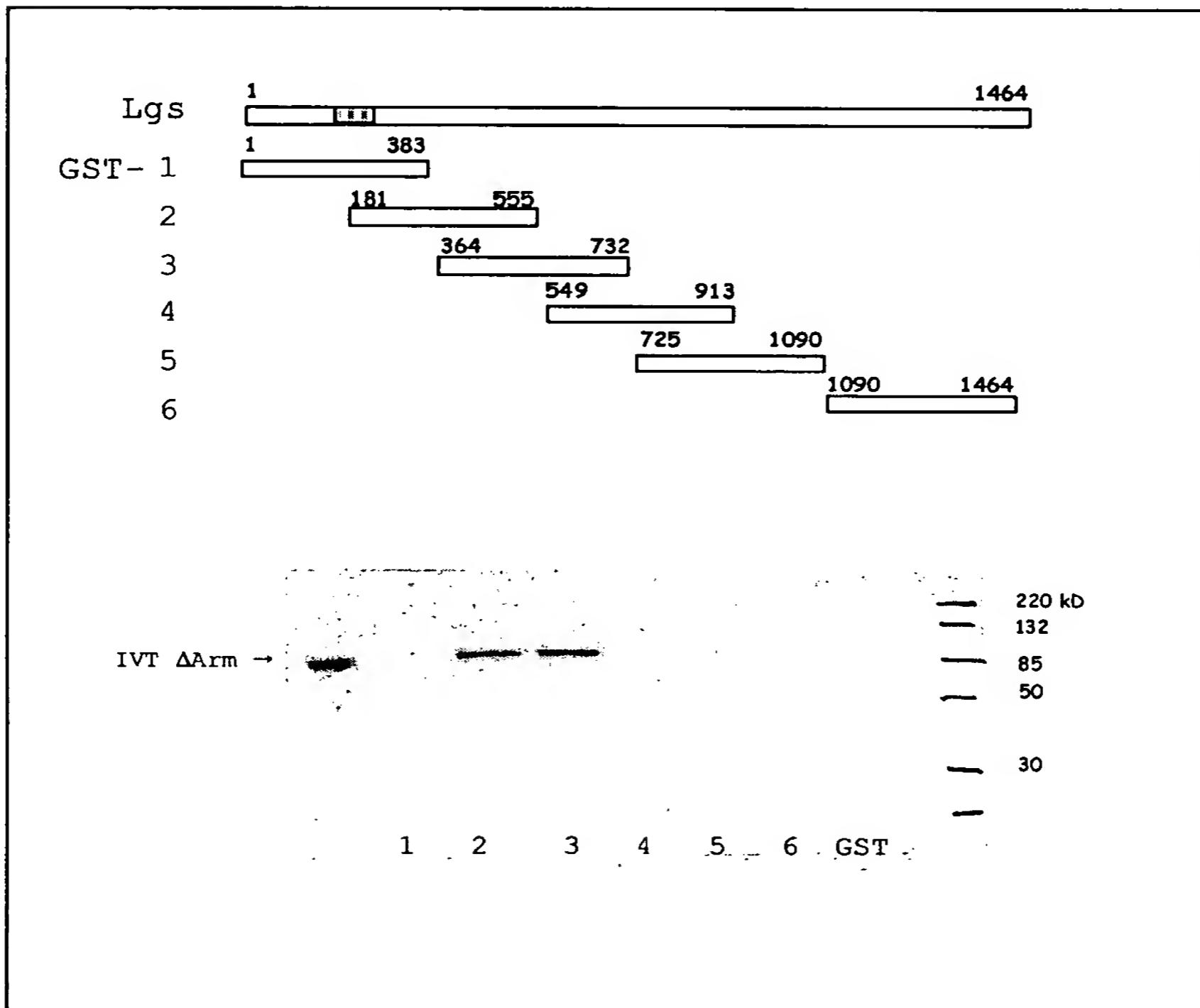
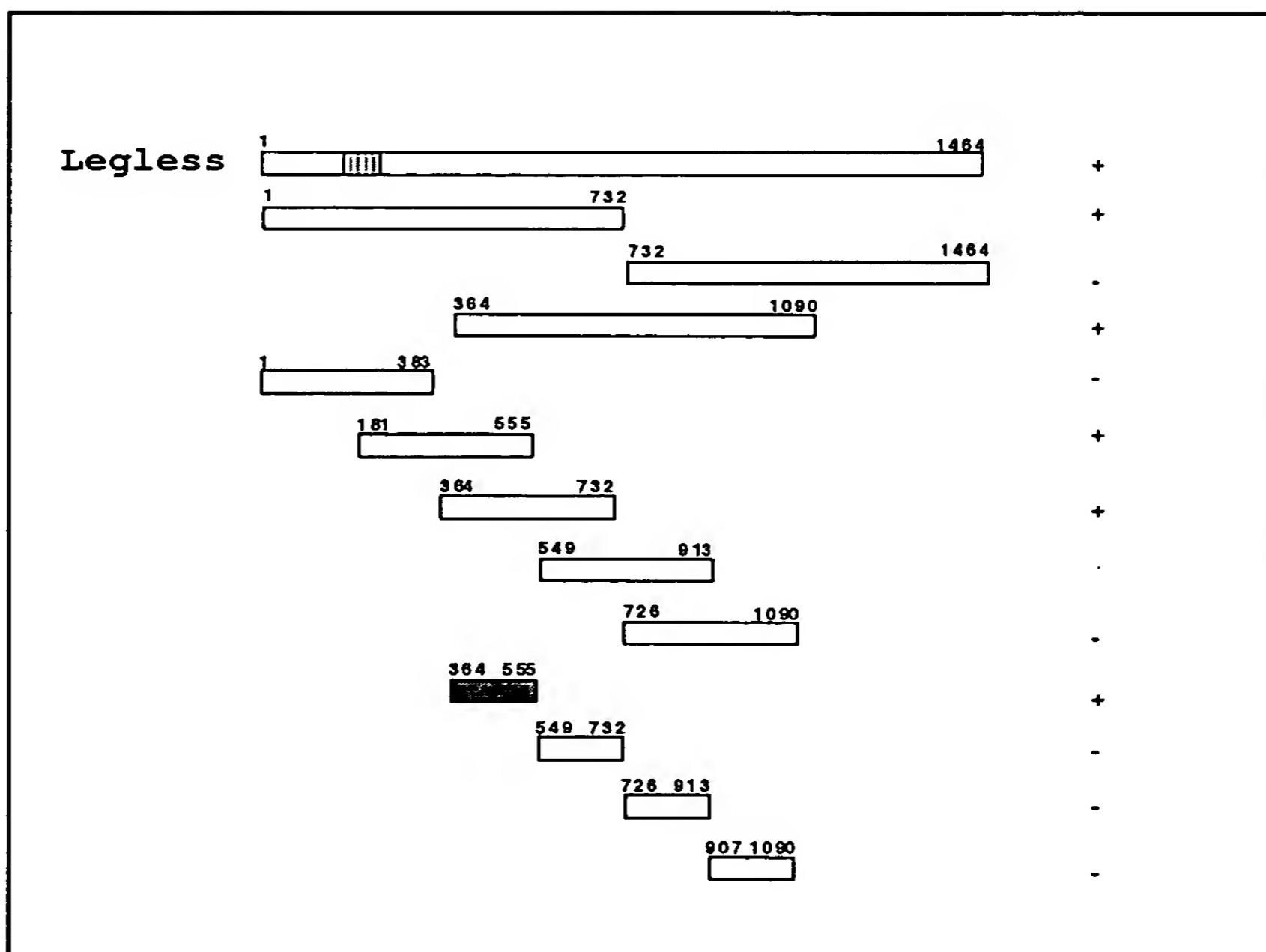


Figure 12B

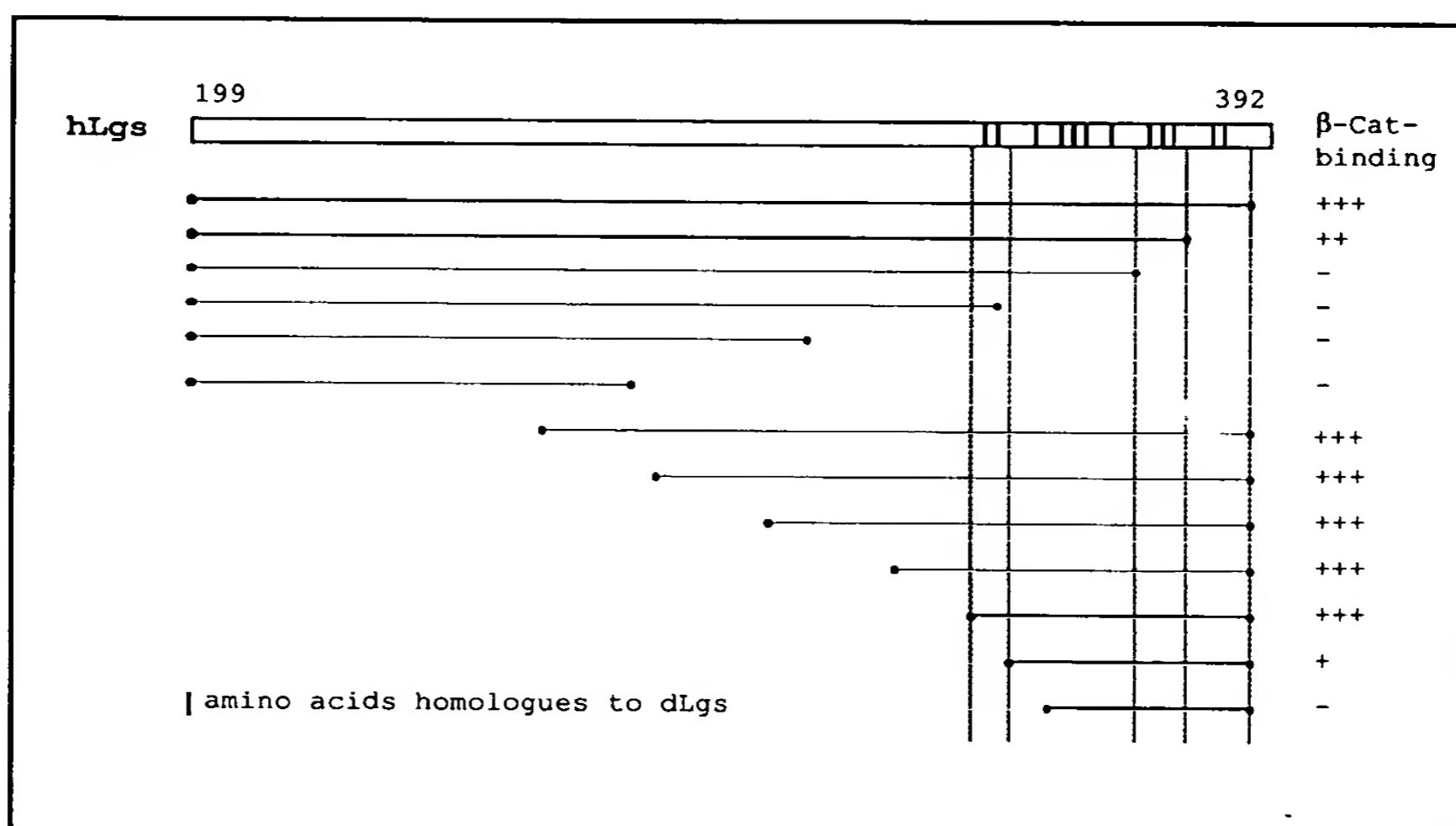
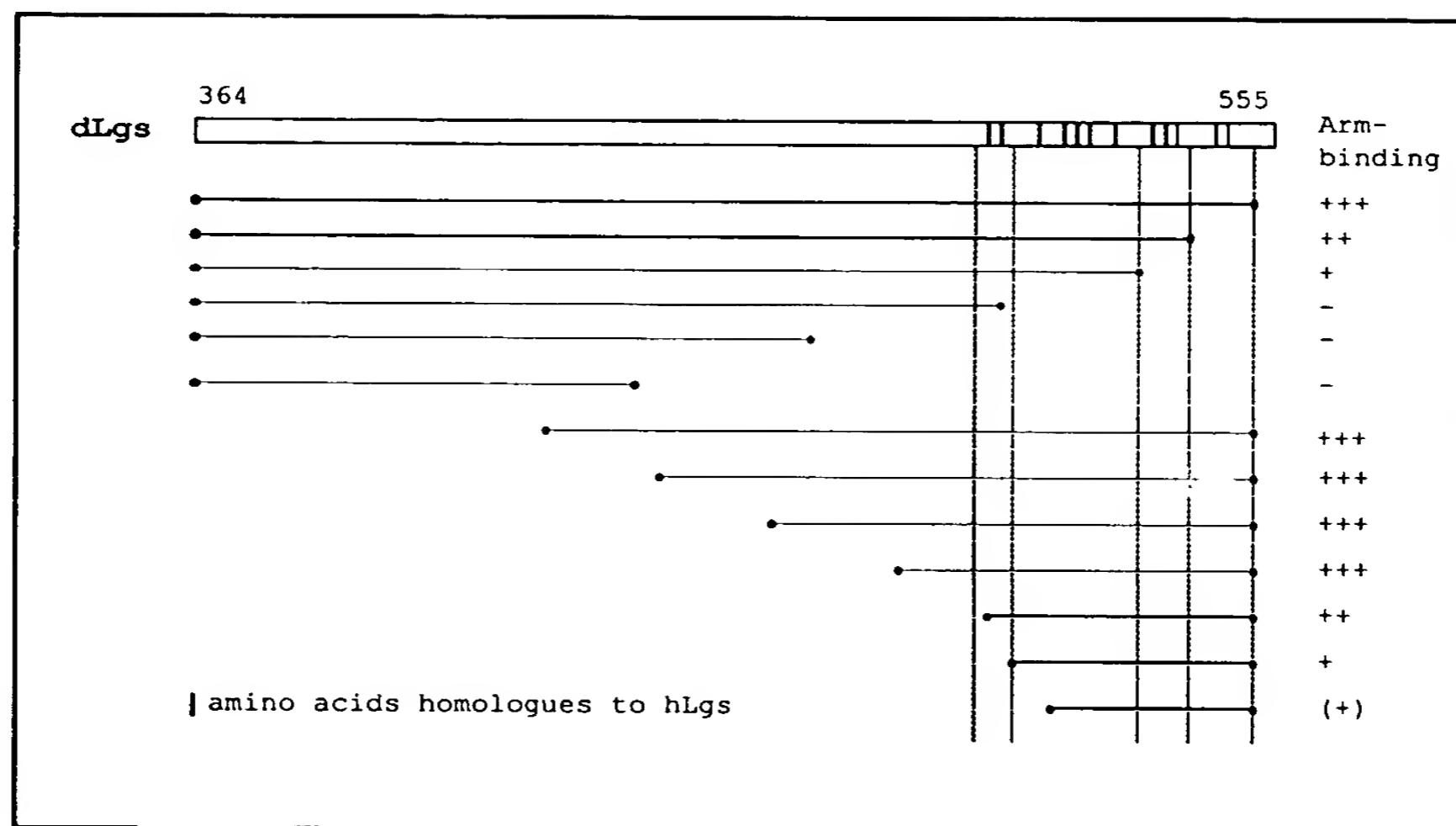


Figure 12C

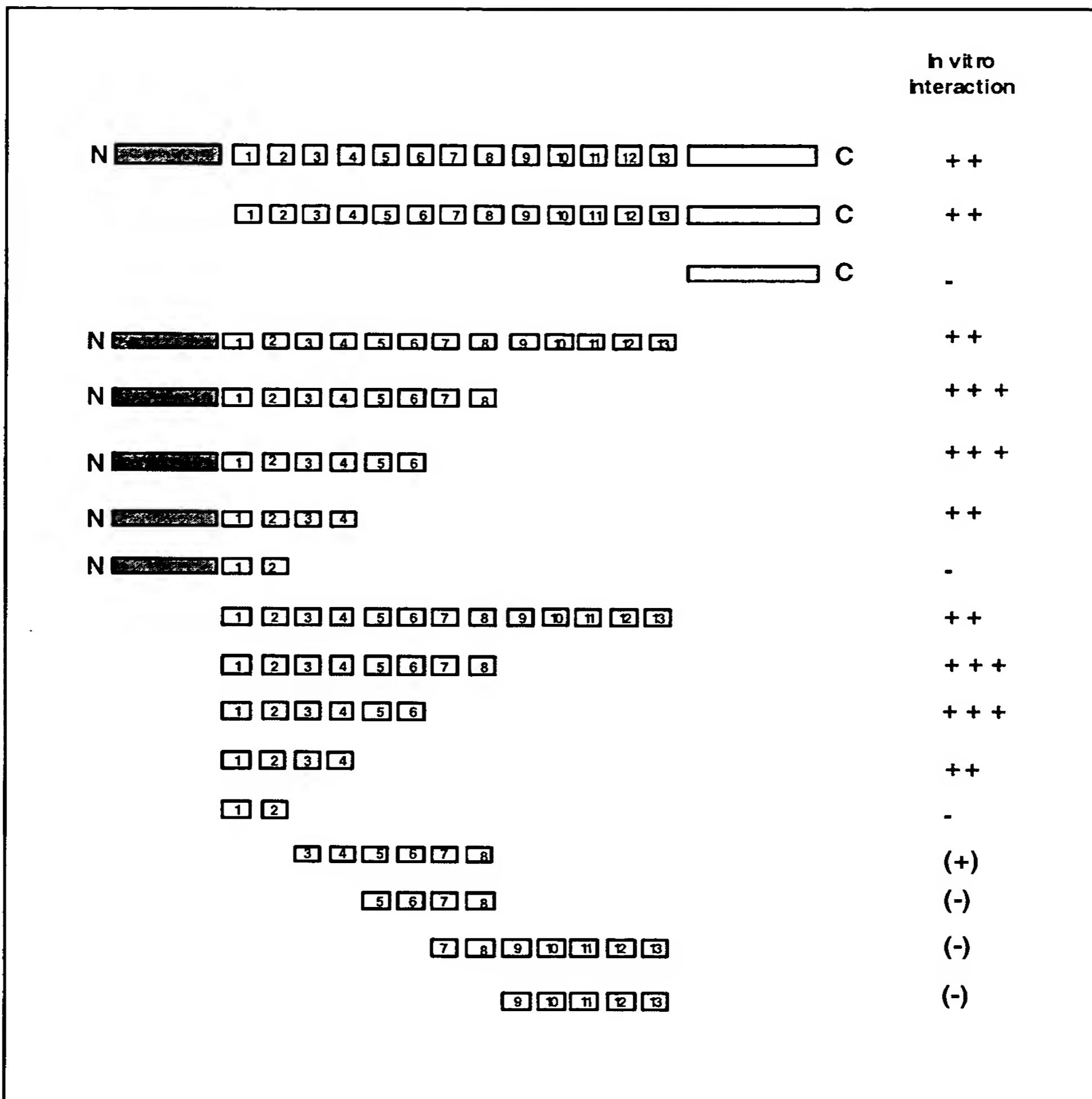
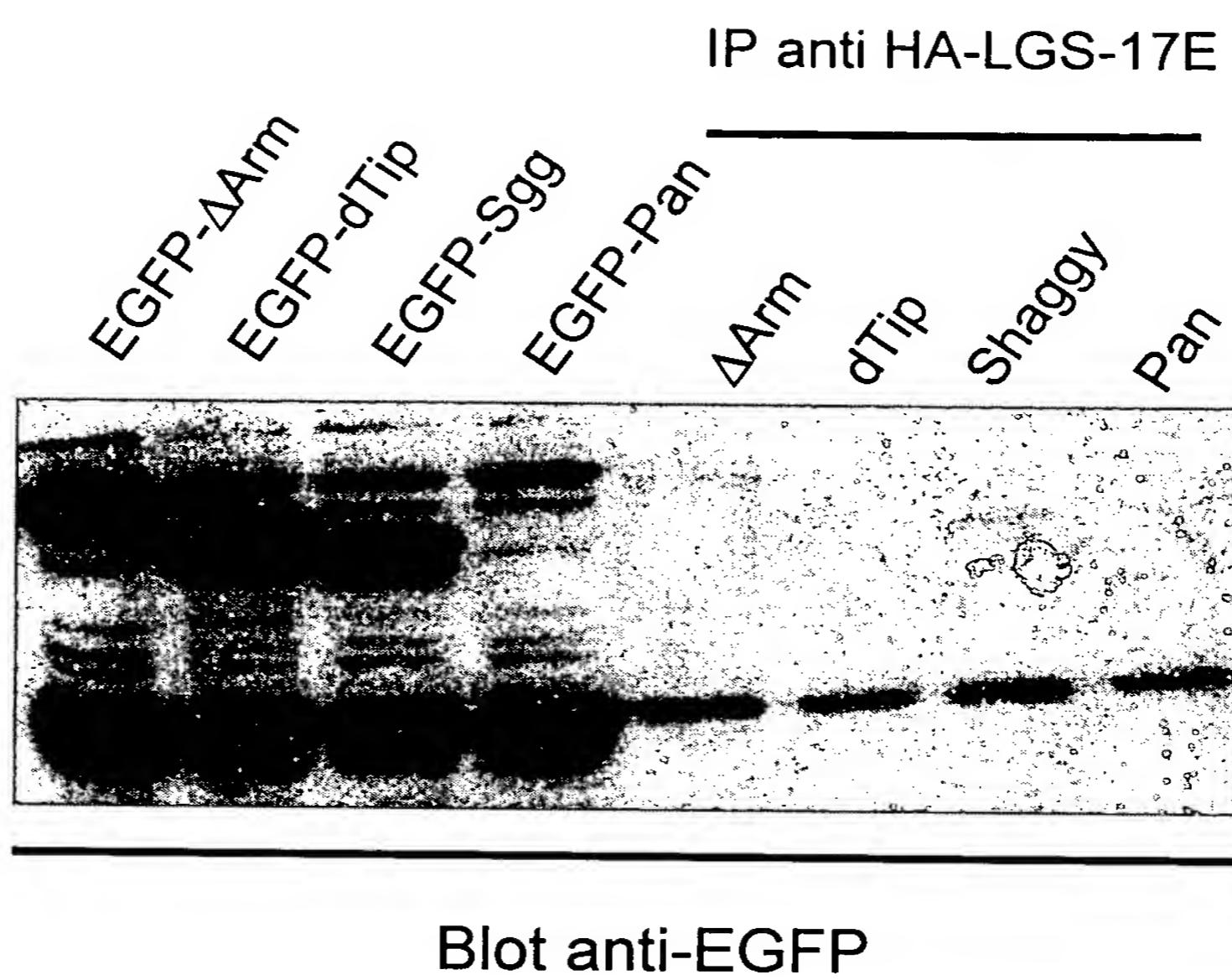


Figure 13

A



B

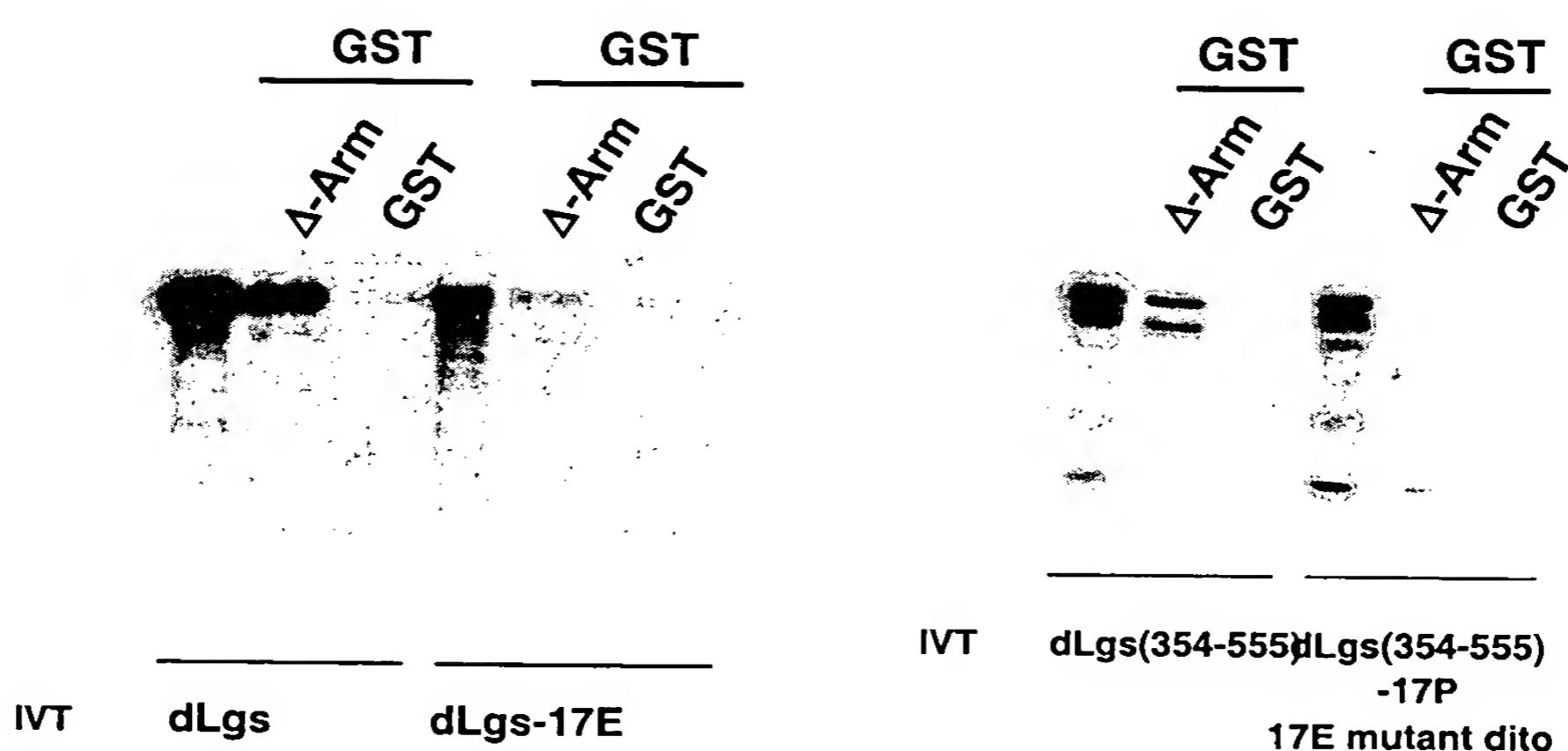
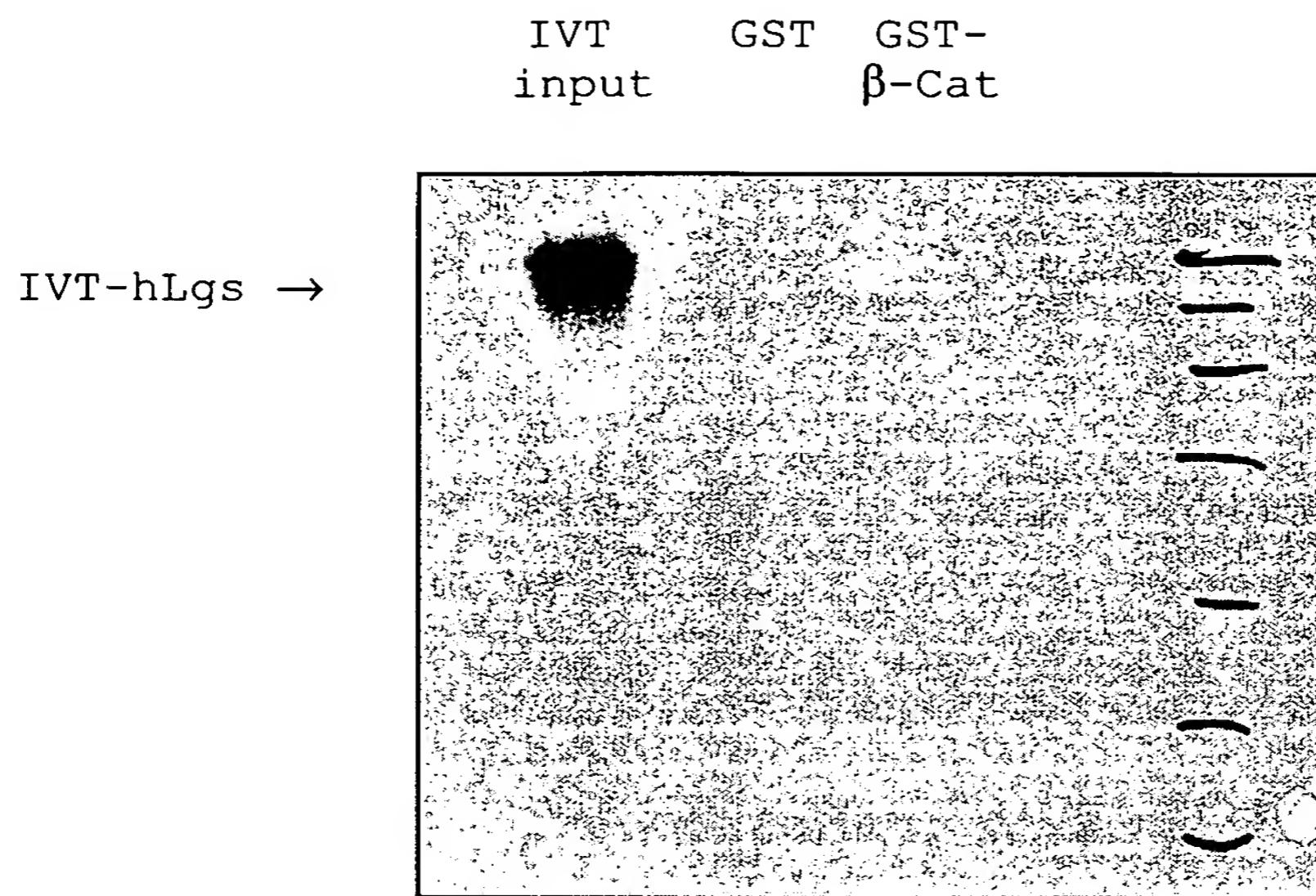


Figure 13

C



D

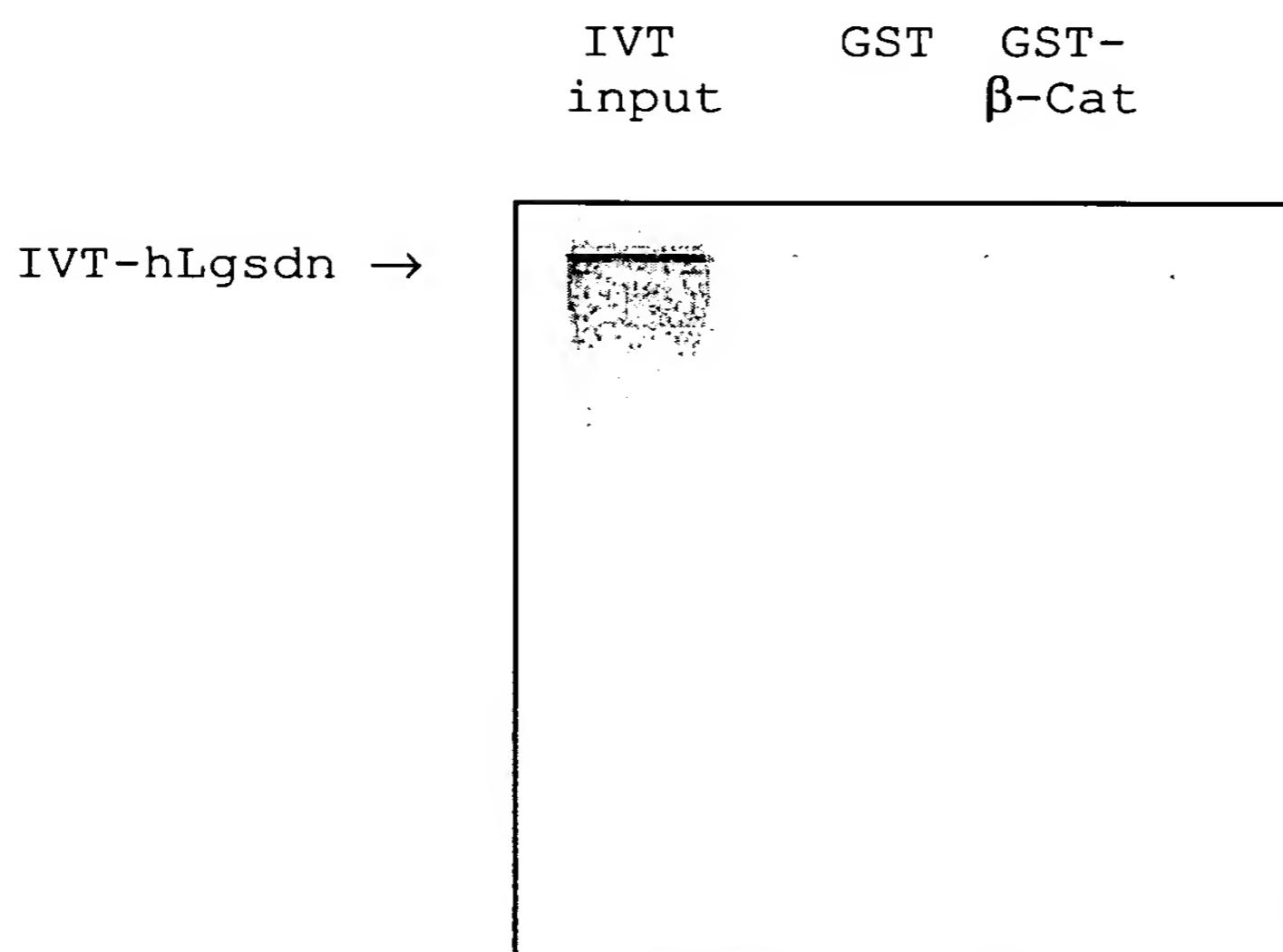
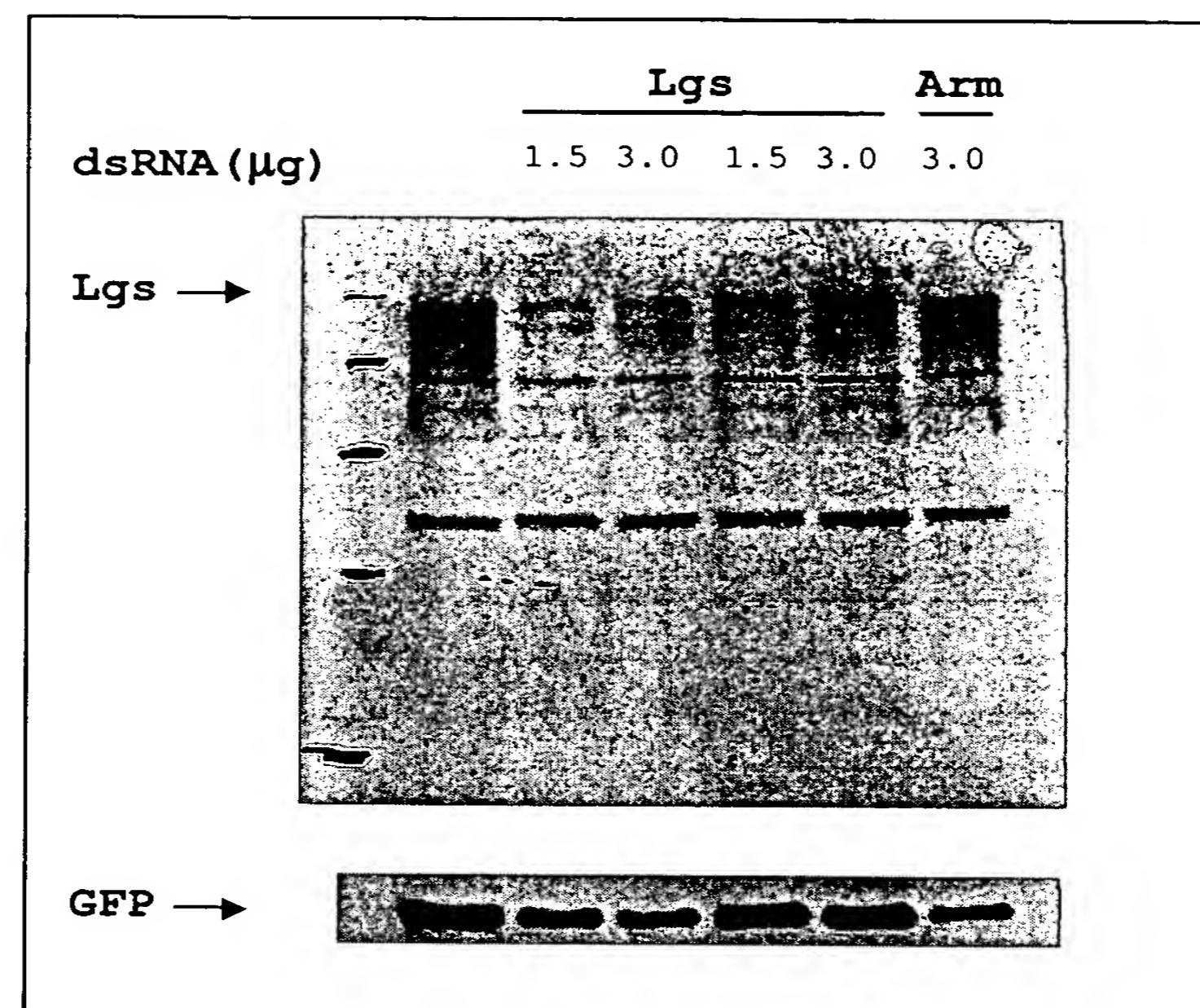
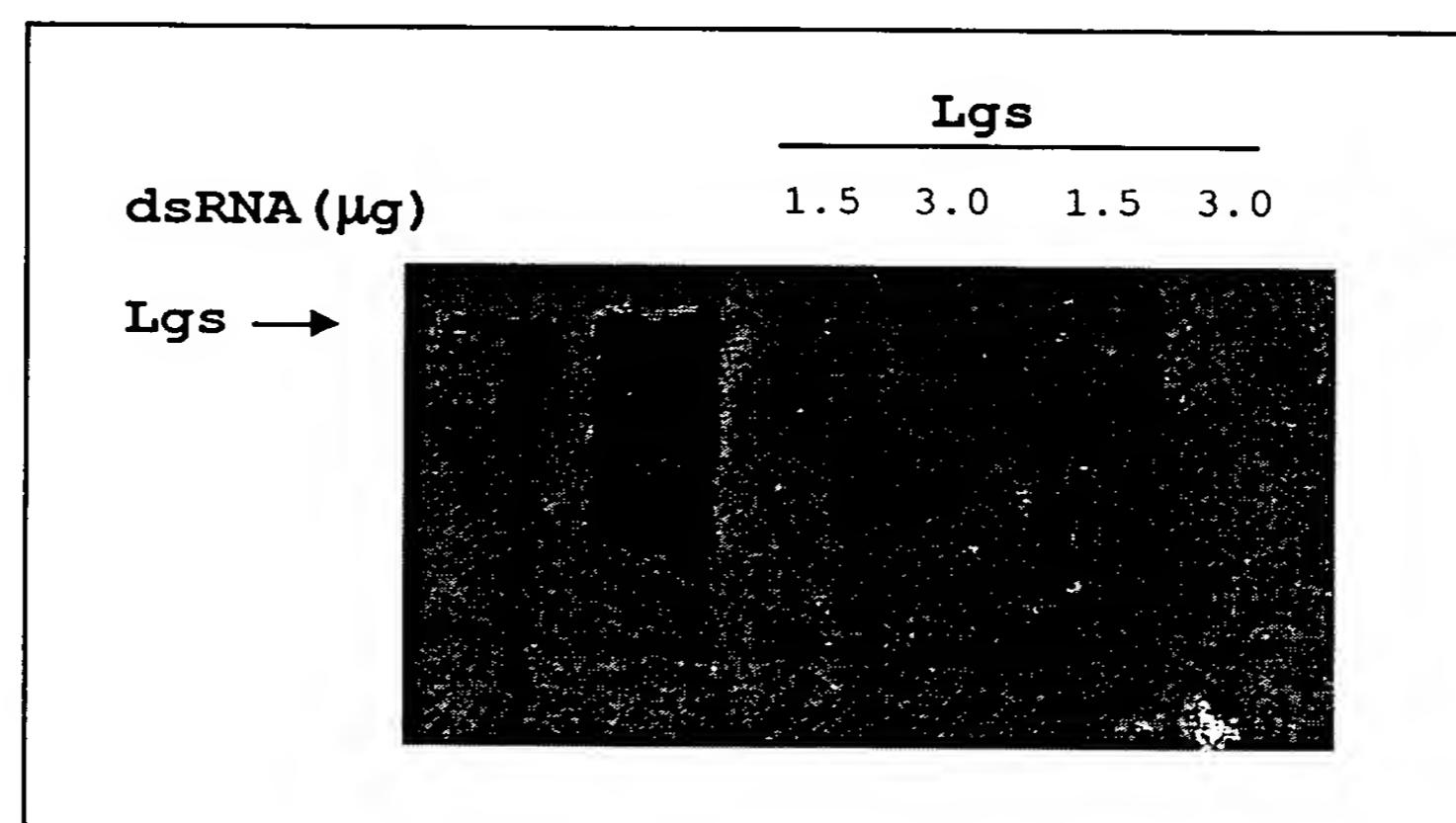


Figure 14



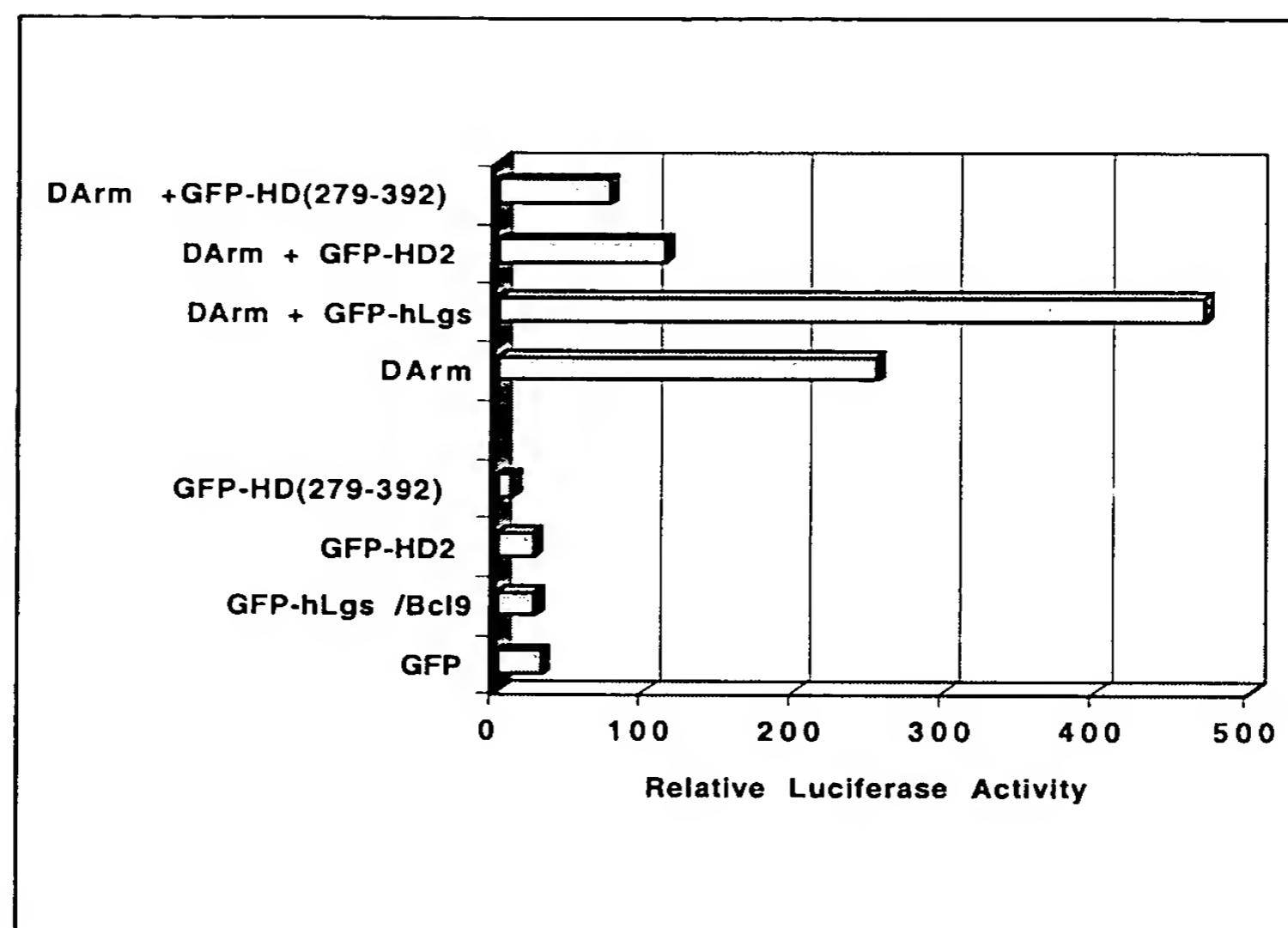
pMT-EGFP (μg) 1.5 1.5 1.5 1.5 1.5 1.5



pMT-dLgs (μg) - 2 2 2 2 2

Figure 15

A



B

